

Form PTO-1449 (modified)		Atty. Docket No. UTSD:64US/MTG	Serial No. 09/684,066
List of Patents and Publications for Applicant's INFORMATION DISCLOSURE STATEMENT (Use several sheets if necessary)		Applicant Rama Ranganathan Steve W. Lockless	
		Filing Date: October 6, 2000	Group: 1645
U.S. Patent Documents <i>See Page 1</i>	Foreign Patent Documents <i>See Page 1</i>	Other Art <i>See Page 1</i>	

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U.S. Patent Documents

Exam. Init.	Ref. Des.	Document Number	Date	Name	Class	Sub Class	Filing Date of App.
LAC	A1	5,523,208	6/4/96	Kohler <i>et al.</i>	435	6	11/30/94

Foreign Patent Documents

Exam. Init.	Ref. Des.	Document Number	Date	Country	Class	Sub Class	Translation Yes/No

Other Art (Including Author, Title, Date Pertinent Pages, Etc.)

Exam. Init.	Ref. Des.	Citation
LAC	C1	Altschul <i>et al.</i> , "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs," <i>Nucl. Acids Res.</i> , 25(17):3389-3402, 1997.
LAC	C2	Atwell <i>et al.</i> , "Structural plasticity in a remodeled protein-protein interface," <i>Science</i> , 278:1125-1128, 1997.
LAC	C3	Bailey and Gribskov, "Combining evidence using p-values: application to sequence homology searches," <i>Bioinformatics</i> , 14(1):48-54, 1998.
LAC	C4	Böhm and Jaenicke, "Correlation functions as a tool for protein modeling and structure analysis," <i>Protein Science</i> , 1:1269-1278, 1992.
LAC	C5	Cabral <i>et al.</i> , "Crystal structure of a PDZ domain," <i>Nature</i> , 382:649-652, 1996.
LAC	C6	Carter <i>et al.</i> , "The use of double mutants to detect structural changes in the active site of the Tyrosyl-tRNA synthetase (<i>Bacillus stearothermophilus</i>)," <i>Cell</i> , 38:835-840, 1984.
LAC	C7	Clackson and Wells, "A hot spot of binding energy in a hormone-receptor interface," <i>Science</i> , 267:383-386, 1995.
LAC	C8	Daniels <i>et al.</i> , "Crystal structure of the hCASK PDZ domain reveals the structure basis of class II PDZ domain target recognition," <i>Nat. Struct. Biol.</i> , 5(4):317-325, 1998.
LAC	C9	Doyle <i>et al.</i> , "Crystal structures of a complexed and peptide-free membrane protein-binding domain: molecular basis of peptide recognition by PDZ," <i>Cell</i> , 85:1067-1076, 1996.

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EXAMINER: *Lori A. Claw*DATE CONSIDERED: *2-24-02*

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Rama Ranganathan
Steve W. LocklessFiling Date:
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1645

U.S. Patent Documents

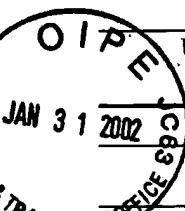
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Foreign Patent Documents

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Other Art

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**Other Art (Including Author, Title, Date Pertinent Pages, Etc.)**

Exam. Init.	Ref. Des.	Citation
JK	C10	Heim and Tsien, "Engineering green fluorescent protein for improved brightness, longer wavelengths and fluorescence resonance energy transfer," <i>Curr. Biol.</i> , 6:178-182, 1996. Article printed from the BioMedNet website, http://journals.bmn.com/journals/list/browse... January 8, 2002.
JK	C11	Feng and Doolittle, "Progressive alignment of amino acid sequences and construction of phylogenetic trees from them," <i>Meth. Enzymology</i> , 266:368-382, 1996.
LAC	C12	Goldstein <i>et al.</i> , "The charybdotoxin receptor of a Shaker K ⁺ channel: peptide and channel residues mediating molecular recognition," <i>Neuron</i> , 12:1377-1388, 1994.
LAC	C13	Hedstrom <i>et al.</i> , "Converting trypsin to chymotrypsin: the role of surface loops," <i>Science</i> , 255:1249-1253, 1992.
LAC	C14	Hedstrom, "Trypsin: a case study in the structural determinants of enzyme specificity," <i>Biol. Chem.</i> , 377:465-470, 1996.
JK	C15	Hidalgo and MacKinnon, "Revealing the architecture of a K ⁺ channel pore through mutant cycles with a peptide inhibitor," <i>Science</i> , 268:307-310, 1995.
JK	C16	Holt and Ackers, "The pathway of allosteric control as revealed by hemoglobin intermediate states," <i>FASEB J.</i> , 9:210-218, 1995.
JK	C17	Hughey and Krogh, "Hidden Markov models for sequence analysis: extension and analysis of the basic method," <i>Comput. Appl. Biosci.</i> , 12(2):95-107, 1996.
JK	C18	Karlin and Brendel, "Chance and statistical significance in protein and DNA sequence analysis," <i>Science</i> , 257:39-49, 1992.
JK	C19	Karlin, "Statistical significance of sequence patterns in proteins," <i>Curr. Opin. Struct. Biol.</i> , 5:360-371, 1995.
JK	C20	Karlin, "Statistical studies of biomolecular sequences: score-based methods," <i>Philos. Trans. R. Soc. Lond. B. Biol. Sci.</i> , 344:325-402, 1994.
JK	C21	Leluk, "A new algorithm for analysis of the homology in protein primary structure," <i>Comput. Chem.</i> , 22(1):123-131, 1998.
JK	C22	LiCata and Ackers, "Long-range, small magnitude nonadditivity of mutational effects in proteins," <i>Biochemistry</i> , 34(10):3133-3139, 1995.

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EXAMINER:

Lee A. Clew

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Form PTO-1449 (modified)

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Rama Ranganathan
Steve W. LocklessFiling Date:
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*See Page 1*Other Art
*See Page 1***Other Art (Including Author, Title, Date Pertinent Pages, Etc.)**

Exam. Init.	Ref. Des.	Citation
LKC	C23	Lichtarge <i>et al.</i> , "An evolutionary trace method defines binding surfaces common to protein families," <i>J. Mol. Biol.</i> , 257:342-358, 1996.
LKC	C24	Lockless and Ranganathan, "Evolutionarily conserved pathways of energetic connectivity in protein families," <i>Science</i> , 286:295-299, 1999.
LKC	C25	Monod <i>et al.</i> , "On the nature of allosteric transitions: a plausible model," <i>J. Mol. Biol.</i> , 12:88-118, 1965.
LKC	C26	Nicholls, <i>et al.</i> , "Protein folding and association: insights from the interfacial and thermodynamic properties of hydrocarbons," <i>Proteins</i> , 11:281-296, 1999.
LKC	C27	Ortiz <i>et al.</i> , "Method for low resolution prediction of small protein tertiary structure," <i>Pacific Symp. On Biocomputing</i> , 316-327, 1997.
LKC	C28	Patten <i>et al.</i> , "The immunological evolution of catalysis," <i>Science</i> , 271:1086-1091, 1996.
LKC	C29	Perona <i>et al.</i> , "Structural origins of substrate discrimination in trypsin and chymotrypsin," <i>Biochemistry</i> , 34:1489-1499, 1995.
LKC	C30	Perry <i>et al.</i> , "Long-range electrostatic interactions can influence the folding, stability, and cooperativity of dihydrofolate reductase," <i>Biochemistry</i> , 28:7961-7968, 1989.
LKC	C31	Pettigrew <i>et al.</i> , "Probing the energetics of proteins through structural perturbation: sites of regulatory energy in human hemoglobin," <i>Proc. Natl. Acad. Sci. USA</i> , 79:1849-1853, 1982.
LKC	C32	Ponting <i>et al.</i> , "PDZ domains: targeting signalling molecules to sub-membranous sites," <i>BioEssays</i> , 19(6):469-479, 1997.
LKC	C33	Ranganathan <i>et al.</i> , "Spatial localization of the K ⁺ channel selectivity filter by mutant cycle-based structure analysis," <i>Neuron</i> , 16:131-139, 1996.
LKC	C34	Sambrook <i>et al.</i> , <i>Molecular Cloning: A Laboratory Manual</i> , 2 nd Ed., Cold Spring Harbor, NY, 1989.
LKC	C35	Schreiber and Fersht, "Energetics of protein-protein interactions: analysis of the Barnase-Barstar interface by single mutations and double mutant cycles," <i>J. Mol. Biol.</i> , 248:478-486, 1995.
LKC	C36	Songyang <i>et al.</i> , "Recognition of unique carboxyl-terminal motifs by distinct PDZ domains," <i>Science</i> , 275:73-77, 1997.

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EXAMINER:

Lee A. Glass

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WAC	C37	Stampe <i>et al.</i> , "Intimations of K ⁺ channel structure from a complete functional map of the molecular surface of charybdotoxin," <i>Biochemistry</i> , 33:443-450, 1994.
LAC	C38	Stroud and Fauman, "Significance of structural changes in proteins: expected errors in refined protein structures," <i>Protein Sci.</i> , 4:2392-2404, 1995.
LAC	C39	Sunyaev <i>et al.</i> , "PSIC: profile extraction from sequence alignments with position-specific counts of independent observations," <i>Protein Eng.</i> , 12(5):387-394, 1999.
WAC	C40	Thompson <i>et al.</i> , "CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice," <i>Nucl. Acids Res.</i> , 22(22):4673-4680, 1994.
LAC	C41	Tolman, <i>The principles of statistical mechanics</i> , Dover Publications Inc., New York, 1938.
WAC	C42	Turner <i>et al.</i> , "Mutagenic dissection of hemoglobin cooperativity: effects of amino acid alteration on subunit assembly of Oxy and Deoxy tetramers," <i>Proteins</i> , 14:333-350, 1992.
LAC	C43	Vingron and Waterman, "Sequence alignment and penalty choice. Review of concepts, case studies and implications," <i>J. Mol. Biol.</i> , 235:1-12, 1994.
WAC	C44	Wells, "Binding in the growth hormone receptor complex," <i>Proc. Natl. Acad. Sci. USA</i> , 93:1-6, 1996.
WAC	C45	Wells, "Structural and functional epitopes in the growth hormone receptor complex," <i>Bio/Technol.</i> , 13:647-651, 1995.

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EXAMINER: <i>Lei A. Cao</i>	DATE CONSIDERED: <i>2-24-02</i>
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